

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Urban, Robert G.
Chicz, Roman M.
Collins, Edward J.
Hedley, Mary Lynn
- (ii) TITLE OF THE INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
PROTEIN
- (iii) NUMBER OF SEQUENCES: 33
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Fish & Richardson, P.C.
 - (B) STREET: 225 Franklin Street
 - (C) CITY: Boston
 - (D) STATE: MA
 - (E) COUNTRY: US
 - (F) ZIP: 02110-2804
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: Windows95
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/169,425
 - (B) FILING DATE: 09-OCT-1998
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/061,657
 - (B) FILING DATE: 09-OCT-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Fraser, Janis K.
 - (B) REGISTRATION NUMBER: 34,819
 - (C) REFERENCE/DOCKET NUMBER: 08191/004002
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 617-542-5070
 - (B) TELEFAX: 617-543-8906
 - (C) TELEX: 200154

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Leu Leu Met Gly Thr Leu Gly Ile Val

1

5

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Thr Leu Gly Ile Val Cys Pro Ile Cys
1 5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG GCC ATA AGT GGA GTC CCT GTG CTA GGA TTT TTC ATC ATA GCT GTG
Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
1 5 10 15

48

CTG ATG AGC GCT CAG GAA TCA TGG GCT GCC CTG ATG GGC ACC CTG GGC 96
 Leu Met Ser Ala Gln Glu Ser Trp Ala Ala Leu Met Gly Thr Leu Gly
 20 25 30

ATC GTG TGC CCC ATC TGC TGA 117
 Ile Val Cys Pro Ile Cys
 35

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
 1 5 10 15
 Leu Met Ser Ala Gln Glu Ser Trp Ala Ala Leu Met Gly Thr Leu Gly
 20 25 30
 Ile Val Cys Pro Ile Cys
 35

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCACTTTTCG	GGGAAATGTG	CGCGGAACCC	CTATTTGTTT	ATTTTCTAA	ATACATTCAA	60
ATATGTATCC	GCTCATGAGA	CAATAACCCT	GATAAATGCT	TCAATAATAT	TGAAAAGGA	120
AGAGTCCTGA	GGCGGAAAGA	ACCAGCTGTG	GAATGTGTGT	CAGTTAGGCT	GTGGAAAGTC	180
CCCAGGCTCC	CCAGCAGGCA	GAAGTATGCA	AAGCATGCAT	CTCAATTAGT	CAGCAACCAG	240
GTGTGGAAAG	TCCCCAGGCT	CCCCAGCAGG	CAGAAGTATG	CAAAGCATGC	ATCTCAATTA	300
GTCAGCAACC	ATAGTCCCGC	CCCTAACTCC	GCCCATCCCG	CCCCTAACTC	CGCCAGTTC	360
CGCCCCATTCT	CCGCCCCATG	GCTGACTAAT	TTTTTTTATT	TATGCAGAGG	CCGAGGCCGC	420
CTCGGCCTCT	GAGCTATTCC	AGAAGTAGTG	AGGAGGCTTT	TTTGGAGGCC	TAGGCTTTTG	480
CAAAGATCGA	TCAAGAGACA	GGATGAGGAT	CGTTTCGCAT	GATTGAACAA	GATGGATTGC	540
ACGCAGGTTT	TCCGGCCGCT	TGGGTGGAGA	GGCTATTTCG	CTATGACTGG	GCACAACAGA	600
CAATCGGCTG	CTCTGATGCC	GCCGTGTTCC	GGCTGTCAGC	GCAGGGGCCG	CCGGTTCTTT	660
TTGTCAAGAC	CGACCTGTCC	GGTGCCTTGA	ATGAAGTCA	AGACGAGGCA	GCGCGGCTAT	720
CGTGGCTGGC	CACGACGGGC	GTTCTTGGC	CAGCTGTGCT	CGACGTTGTC	ACTGAAGCGG	780
GAAGGGACTG	GCTGCTATTG	GGCGAAGTGC	CGGGGCAGGA	TCTCCTGTCA	TCTCACCTTG	840
CTCCTGCCGA	GAAAGTATCC	ATCATGGCTG	ATGCAATGCG	GCGGCTGCAT	ACGCTTGATC	900
CGGCTACCTG	CCCATTCGAC	CACCAAGCGA	AACATCGCAT	CGAGCGAGCA	CGTACTCGGA	960
TGGAAGCCGG	TCTTGTCGAT	CAGGATGATC	TGGACGAAGA	GCATCAGGGG	CTCGCGCCAG	1020
CCGAAGTGT	CGCCAGGCTC	AAGGCGAGCA	TGCCCGACGG	CGAGGATCTC	GTCGTGACCC	1080
ATGGCGATGC	CTGCTTGCCG	AATATCATGG	TGGAAAATGG	CCGCTTTTCT	GGATTCATCG	1140
ACTGTGGCCG	GCTGGGTGTG	GCGGACCGCT	ATCAGGACAT	AGCGTTGGCT	ACCCGTGATA	1200
TTGCTGAAGA	GCTTGGCGGC	GAATGGGCTG	ACCGCTTCCT	CGTGCTTTAC	GGTATCGCCG	1260
CTCCCGATTG	GCAGCGCATC	GCCTTCTATC	GCCTTCTTGA	CGAGTTCTTC	TGAGCGGGAC	1320

TCTGGGGTTC	GAAATGACCG	ACCAAGCGAC	GCCCAACCTG	CCATCACGAG	ATTTCGATTC	1380
CACCGCCGCC	TTCTATGAAA	GGTTGGGCTT	CGGAATCGTT	TTCCGGGACG	CCGGCTGGAT	1440
GATCCTCCAG	CGCGGGGATC	TCATGCTGGA	GTTCTTCGCC	CACCCTAGGG	GGAGGCTAAC	1500
TGAAACACGG	AAGGAGACAA	TACCGGAAGG	AACCCGCGCT	ATGACGGCAA	TAAAAAGACA	1560
GAATAAAACG	CACGGTGTTC	GGTCGTTTGT	TCATAAACGC	GGGGTTCGGT	CCCAGGGCTG	1620
GCACTCTGTC	GATACCCAC	CGAGACCCCA	TTGGGGCCAA	TACGCCCGCG	TTTCTTCCCT	1680
TTCCCCACCC	CACCCCCCAA	GTTCCGGTGA	AGGCCCAGGG	CTCGCAGCCA	ACGTCGGGGC	1740
GGCAGGCCCT	GCCATAGCCT	CAGGTTACTC	ATATATACTT	TAGATTGATT	TAAAACTTCA	1800
TTTTTAATTT	AAAAGGATCT	AGGTGAAGAT	CCTTTTTTGT	AATCTCATGA	CCAAAATCCC	1860
TTAACGTGAG	TTTTCGTTCC	ACTGAGCGTC	AGACCCCGTA	GAAAAGATCA	AAGGATCTTC	1920
TTGAGATCCT	TTTTTTCTGC	GCGTAATCTG	CTGCTTGCAA	ACAAAAAAC	CACCGCTACC	1980
AGCGGTGGTT	TGTTTGCCGG	ATCAAGAGCT	ACCAACTCTT	TTCCGAAGG	TAAGTGGCTT	2040
CAGCAGAGCG	CAGATACCAA	ATACTGTTCT	TCTAGTGTAG	CCGTAGTTAG	CCCACCACCT	2100
CAAGAACTCT	GTAGCACCGC	CTACATACCT	CGCTCTGCTA	ATCCTGTTAC	CAGTGGCTGC	2160
TGCCAGTGGC	GATAAGTCGT	GTCTTACCGG	GTTGGACTCA	AGACGATAGT	TACCGGATAA	2220
GGCGCAGCGG	TCGGGCTGAA	CGGGGGGTTT	GTGCACACAG	CCCAGCTTGG	AGCGAACGAC	2280
CTACACCCAA	CTGAGATACC	TACAGCGTGA	GCTATGAGAA	AGCGCCACGC	TTCCCGAAGG	2340
GAGAAAGGCG	GACAGGTATC	CGTAAGCGG	CAGGGTCGGA	ACAGGAGAGC	GCACGAGGGA	2400
GCTTCCAGGG	GGAAACGCCT	GGTATCTTTA	TAGTCCTGTC	GGGTTTCGCC	ACCTCTGACT	2460
TGAGCGTCGA	TTTTTGTTGAT	GCTCGTCAGG	GGGGCGGAGC	CTATGGAAAA	ACGCCAGCAA	2520
CGCGGCCTTT	TTACGGTTCC	TGGCCTTTTG	CTGGCCTTTT	GCTCACATGT	TCTTTCTGTC	2580
GTTATCCCTT	GATTCTGTGG	ATAACCGTAT	TACCGCCATG	CATTAGTTAT	TAATAGTAAT	2640
CAATTACGGG	GTCAATTAGT	CATAGCCCAT	ATATGGAGTT	CCGCGTTACA	TAACCTACGG	2700
TAAATGGCCC	GCCTGGCTGA	CCGCCCAACG	ACCCCGCCCC	ATTGACGTCA	ATAATGACGT	2760
ATGTTCCCAT	AGTAACGCCA	ATAGGGACTT	TCCATTGACG	TCAATGGGTG	GAGTATTTAC	2820
GGTAAACTGC	CCACTTGGCA	GTACATCAAG	TGTATCATAT	GCCAAGTACG	CCCCCTATTG	2880
ACGTCAATGA	CGGTAAATGG	CCGCGCTGGC	ATTATGCCCA	GTACATGACC	TTATGGGACT	2940
TTCCTACTTG	GCAGTACATC	TACGTATTAG	TCATCGCTAT	TACCATGGTG	ATGCGGTTTT	3000
GGCAGTACAT	CAATGGGCGT	GGATAGCGGT	TTGACTCACG	GGGATTTCCA	AGTCTCCACC	3060
CCATTGACGT	CAATGGGAGT	TTGTTTTGGC	ACCAAATCA	ACGGGACTTT	CCAAAATGTC	3120
GTAACAACTC	CGCCCCATTG	ACGCAAATGG	GCGGTAGGCG	TGTACGGTGG	GAGGTCTATA	3180
TAAGCAGAGC	TGGTTTAGTG	AACCGTCAGA	TCCGCTAGAG	CTTGCTTGTT	CTTTTTGCAG	3240
AAGCTCAGAA	TAAACGCTCA	ACTTTGGCAG	ATCCGCGGCT	CGAGCCACCA	TGGACATGGC	3300
CATAAGTGGG	GTCCCTGTGC	TAGGATTTTT	CATCATAGCT	GTGCTGATGA	GCGCTCAGGA	3360
ATCATGGGCT	GCCCTGATGG	GCACCCTGGG	CATCGTGTGC	CCCATCTGCT	GAGCTCCTGG	3420
AATTCGGATC	TGGTTACCAC	TAAACCAGCC	TCAAGAACAC	CCGAATGGAG	TCTCTAAGCT	3480
ACATAATACC	AACTTACACT	TTACAAAATG	TTGTCCCCCA	AAATGTAGCC	ATTTCGTATCT	3540
GCTCCTAATA	AAAAGAAAGT	TTCTTCACAT	TCTAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	3600
AAAAAACCCC	CCCCCCCCCC	CCCCATCGAT	TTTCCACCCG	GGTGGGGTAC	CAGGTAAGTG	3660
TACCCAATTC	GCCCTATAGT	GAGTCGTATT	ACAATTCACT	GGCCGTCGTT	TTACAACGTC	3720
GTGACTGGGA	AAACCCTGGC	GTTACCCAAA	TTAATCGCCT	TGCAGCACAT	CCCCCTTTTCG	3780
CCAGCTGGCG	TAATAGCGAA	GAGGCCCGCA	CCGATCGCCC	TTCCCAACAG	TTGCGCAGCC	3840
TGAATGGCGA	ATGGAGATCC	AATTTTTAAG	TGTATAATGT	GTTAAACTAC	TGATTCTAAT	3900
TGTTTGTGTA	TTTTAGATTG	ACAGTCCCAA	GGCTCATTTC	AGGCCCTCA	GTCTCTACAG	3960
TCTGTTTCATG	ATCATAATCA	GCCATACCAC	ATTTGTAGAG	GTTTTACTTG	CTTTAAAAAA	4020
CCTCCACAC	CTCCCCCTGA	ACCTGAAACA	TAAAATGAAT	GCAATTGTTG	TTGTAACTT	4080
GTTTATTGCA	GCTTATAATG	GTTACAAATA	AAGCAATAGC	ATCACAAATT	TCACAAATAA	4140
AGCATTTTTT	TCACTGCATT	CTAGTTGTGG	TTTGTCCAAA	CTCATCAATG	TATCTTAACG	4200
CGTAAATTGT	AAGCGTTAAT	ATTTTGTTAA	AATTCGCGTT	AAATTTTTGT	TAAATCAGCT	4260
CATTTTTTAA	CCAATAGGCC	GAAATCGGCA	AAATCCCTTA	TAAATCAAAA	GAATAGACCG	4320
AGATAGGGTT	GAGTGTGTTT	CCAGTTTGGA	ACAAGAGTCC	ACTATTAAAG	AACGTGGACT	4380
CCAACGTCAA	AGGGCGAAAA	ACCGTCTATC	AGGGCGATGG	CCCACTACGT	GAACCATCAC	4440
CCTAATCAAG	TTTTTTGGGG	TCGAGGTGCC	GTAAGCACT	AAATCGGAAC	CCTAAAGGGA	4500
GCCCCCGATT	TAGAGCTTGA	CGGGGAAAGC	CGGCGAACGT	GGCGAGAAAG	GAAGGGAAGA	4560
AAGCGAAAGG	AGCGGGCGCT	AGGGCGCTGG	CAAGTGTAGC	GGTCACGCTG	CGCGTAACCA	4620
CCACACCCGC	CGCGCTTAAT	GCGCCGCTAC	AGGGCGCGTC	AGGTG		4665

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGCGTCGACA TGGCCATAAG TGGAGTC

27

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAAGCTGGCA GCCCATGATT CCTGAGC

27

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TCATGGGCTG CCAGCTTCGA GGCCCG

27

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGGGAATTCT TAGGCCTTGT CCACGGC

27

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATCAGCGCTC AGGAATCATG GGCTGCCCTG GGCATCGTGT GCCCCATCTG CTGAGCTCGA 60
G 61

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGGGATCCGA ATTCCTCGAG CTCA 24

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATCAGCGCTC AGGAATCATG GGCTCTGATG GGCACCCTGG GCATCGTGTG CCCCATCTGC 60
TGAGCTCGAG 70

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGGGATCCGA ATTCCTCGAG CTCA 24

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Tyr Met Leu Asp Leu Gln Pro Glu Thr
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
1 5 10 15
Leu Met Ser Ala Gln Glu Ser Trp Ala
20 25

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: where Xaa at position 1 is Met, Ala, Ser, Arg, Lys, Gly, Gln, Asp, or Glu

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Xaa Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Thr Leu Gly Ile Val Cys Pro Ile
1 5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gly Thr Leu Gly Ile Val Cys Pro Ile
1 5

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ile Val Cys Pro Ile Cys Ser Gln Lys
1 5

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Lys Asp Glu Leu
1

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Gly Ile Leu Gly Phe Val Phe Thr Leu
1 5

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln Lys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Gly Ile Val Cys Pro Ile Cys
1 5

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: where Xaa at position 1 is Met, Ala, Ser, Arg, Lys, Gly, Gln, Asp, or Glu

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Xaa Thr Leu Gly Ile Val Cys Pro Ile
1 5

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Gly Thr Leu Gly Leu Gly Ile Val Cys Pro Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Lys Phe Glu Arg Gln
1 5

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Gln Phe Glu Phe Lys
1 5

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: where Xaa at position 1 is Met, Ala, Ser, Arg, Lys, Gly, Gln, Asp, or Glu

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Xaa Gly Thr Leu Gly Ile Val Cys Pro Ile Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys
1 5 10